Amendments to the Specification

Please amend Table 1 on page 26 to read as follows

Table 1 on page 26 is amended as follows:

Marker	Oligonucleotide Primer Sequence*	Ref.
HXB**	ATAGCCAAAGAGAGGTGCCC (SEQ ID NO:1) AGAGCCCTTCTGTCTTTTCC (SEQ ID NO:2)	1
D9S127**	CCCTCAAAATTGCTGTCTAT (SEQ ID NO:3) AGATTGATTGATACAAGGATTTG (SEQ ID NO:4)	2
D9S58**	CCTGAGTAGCCGGGACTATA (SEQ ID NO:5) TAGGCAACACATCAAGATCCT (SEQ ID NO:6)	3
D9S59**	AAGGGAATTCATCCCCTGCT (SEQ ID NO:7) TTACACTATACCAAGACTCC (SEQ ID NO:8)	3
ASS	GGTTGGCCTAAGAAAACCAT (SEQ ID NO:9) TGGGGAGCTATAAAAATGAC (SEC ID NO:10)	3
D9S66	CAGACCAGGAATGCATGAAG (SEQ ID NO:11) CACGGGCACACATGTATGC (SEQ ID NO:12)	3
D9S15	TAAAGATTGGGAGTCAAGTA (SEQ ID NO:13) TTCACTTGATGGTGGTAATC (SEQ ID NO:14)	3
D9S53**	GCTGCATACTTTAAACTAGC (SEQ ID NO:15) GGAATATGTTTTTATTAGCTTG (SEQ ID NO:16)	4
D9S105**	GATCATATTGCTTACAACCC (SEQ ID NO:17) ACTTACTCATTAAATCTAGGG (SEQ ID NO:18)	4
D9S109**	GCACAGGCTGCAATATAGAC (SEQ ID NO:19) TTTACTGTATAAAAACTGAAGCTAATA (SEQ ID NO:20)	5
D9S106**	ATTGTGTTGAAATTTGACCCCT (SEQ ID NO:21) CCAGGCTTATTTCCACACCT (SEQ ID NO:22)	4
ABL	TTTACACCTTCACCCAGAGA (SEQ ID NO:23) GGCTGTGTTCAGTTAAACGT (SEQ ID NO:24)	3
GSN**	CAGCCAGCTTTGGAGACAAC (SEQ ID NO:25) TCGCAAGCATATGACTGTAA (SEQ ID NO:26)	6

The bridging paragraph beginning on page 37, line 28, is amended as follows:

Therefore, yet another embodiment of this invention relates to nucleic acid sequences encoding oligonucleotides useful for detecting markers or polymorphisms linked to the familial dysautonomia gene. In particular this embodiment of the invention relates to oligonucleotides encoding flanking regions of repeat sequences which are used as primers for the polymerase chain reaction (PCR). Amplification of DNA with these primers allows for the detection of the polymorphisms D9S309 and D9S310. Such oligonucleotides may be about 15 to about 40 base[s] pairs in length, preferably about 17 to about 25 base pairs in length. In a preferred embodiment the oligonucleotide primers used are 5'–GCCTGGGCAAACAGAGAC–3' (SEQ ID NO: 27), 5'–GCAACTTATTGTTTAACCTG–3' (SEQ ID NO: 28) for the *D9S310* polymorphism and 5'–TAGAGCTCTACCCCCCAAC–3' (SEQ ID NO: 29), 5'–TGAACAGCTATATATGCCATCC–3' (SEQ ID NO: 30) for the *D9S309* polymorphism. It will be understood by one of skill in the art that variations in the D9S309 and the D9S310 oligonucleotide primers may be made but still result in nucleic acid sequences capable of amplifying those sequences. These oligonucleotide primers may be used in the methods described herein for detecting the presence in a subject of the D9S309 and D9S310 polymorphisms which are linked to the FD gene.

The paragraph on page 38, line 23, is amended as follows:

Two additional markers designated D9S172 and D9S174 were tested and demonstrated to be linked to the familial dysautonomia gene. D9S174 is approximately 2 cM distal to D9S58 and D9S172 is estimated to be about 3 – 4 cM proximal to D9S58. The oligonucleotide primer sequences encoding the flanking regions of the D9S172 and D9S174 polymorphisms are as follows: D9S172: 5'–AACTACAGTGTTCAGTGTGGTG–3' (SEQ ID NO: 31), 5'–ATGGGAATGAGTAGCAAACA–3' (SEQ ID NO: 32) and D9S174: 5'–TCCAAAGTTCCCCAGGTG–3' (SEQ ID NO: 33), 5'–GTGTTTAATGACCCTTGTGGCTAC–3' (SEQ ID NO: 34) (Weissenbach, T., et al. (1992) Nature 359:794-801. The location of the FD gene can now be further restricted by markers *D9S172* and *D9S105* to within 6 cM, i.e., 6 million nucleotides around DS958.